This paper is filed in response to the outstanding Office action in the above-referenced application and Applicants believe that with this response all remaining issues in the case have been addressed Applicants respectfully request entry of these remarks in the prosecution history of the present case prior to further substantive action.

I. Cancellation of claims 36-41

Please cancel claims 36-41 as being drawn to non-elected subject matter. Applicants reserve the right to pursue these claims in further divisional application(s).

For the Examiner's convenience and pursuant to the requirements of 37 C.F.R. §1.121 a complete list of the claims is attached above.

II. Response to rejection under 35 U.S.C. §112, second paragraph

Claims 1, 2, 20 and 22 and dependent claims therefrom were rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to point out and distinctly claim the subject matter of the invention. More particularly, the Examiner queried the use of the term "information regions of the probes," requesting clarification of what is intended by the use of this term. Applicants point to the specification, which beginning on page 13, line 20 teaches the rules for determining the information region comprises and how the consensus is defined. That section of the specification states:

> The invention further provides a set of pools of probes wherein each probe comprises an information region . . . wherein the set of the pools of probes also satisfies one or more of the following *rules describing the information regions of the probes*, said rules selected from the group consisting of: (a) a consensus sequence of at least one pool in the set consists only of the letters selected from the group consisting of V, H, D, B, and N as defined in Table A below; (b) a consensus sequence of probes in each pool in the set comprises more than three different letters selected from the group consisting of A, C, G, T, U, M, R, W, S, Y, K, V, H, D, B, and N as defined in Table A below; (c) consensus sequences from each informative

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position of all pools in the set comprise more than eight letters selected from the group consisting of A, C, G, T, U, M, R, W, S, Y, K, V, H, D, B, and N as defined in Table A below; and (d) consensus sequences from each information region of all pools in the set comprise more than five different letters selected from the group consisting of A, C, G, T, U, M, R, W, S, Y, K, V, H, D, B, and N and at least one of the five letters is selected from the group consisting of M, R, W, S, Y, and K as defined in Table A below. A consensus sequence is determined by alignment of bases in probes within or among pools limiting degeneracy at each aligned position to either one, two, three or four possible bases at that position. Letter coding for all levels of degeneracy are shown in Table A. Alternatively, rules for the set may be selected from the group consisting of (a) no two probes of length K within the pool overlap by K-1 bases; (b) no two probes pools within a pool are reverse complements; (c) less than 50% of the probes in the set are repeated in any two pools within the set; (d) when two or more probes in a pool vary at a nucleotide position, there are no more than three different bases at that varied position; (e)no two probes in a pool overlap by a significant number of bases; and (e) there exists at least one nucleotide position wherein all probes within the pool are identical.

In addition, the specification at page 18, lines 13-24, states that:

The length of the probes described above and throughout the specification *refers to the length of the informational content (i.e., the information region or the informative region) of the probes, not necessarily the actual physical length of the probes*. The probes used in SBH frequently contain degenerate ends that do not contribute to the information content of the probes. For example, SBH applications frequently use mixtures of probes of the formula NxByNz, wherein N represents any of the four nucleotides and varies for the polynucleotides in a given mixture, B represents any of the four nucleotides but is the same for each of the polynucleotides in a given mixture, and x, y, and z are all integers. Preferably, x is an integer between 0 and 5, y is an integer between 4 and 20, and z is an integer between 0 and 5. Hybridization discrimination of mismatches in these degenerate probe mixtures refers only to the length of the informational content, not the full physical length.

Given these teachings in the specification, Applicants submit that it should be understood that the "information region of the probes" is that region of the

probe that that excludes the degenerate ends but includes an informative region that is calculated using the rules detailed at page 13 of the specification.

Applicants believe the above-quoted sections of the specification clarify what is intended by the term "information regions of the probes," and therefore Applicants request that the rejection be withdrawn and the claims be reconsidered for allowance.

The Examiner is invited to contact the undersigned with any questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,
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